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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2009; month=3; day=24; hr=15; min=1; sec=14; ms=491; ]

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\*\*\*\*\*

Reviewer Comments:

<210> 8

<211> 139

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: partial  
sequence of pGEX2ThCD83ext

<400> 8

Per the above sequence id# 8, please insert <220>, whenever numeric identifiers <221>, <222> or <223> is present. Please correct the remaining sequences showing similar errors. Please also correct <160> response, there were a total of 13 sequences found not 12.

Ser Pro Asn Lys His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu

195

200

205

Val

209

The above is a sample of invalid amino acid numbering also appearing in sequence id# 13. Please number amino acids every 5th base.

\*\*\*\*\*



Application No: 10535522 Version No: 2.0

**Input Set:**

**Output Set:**

**Started:** 2009-03-02 13:23:43.501  
**Finished:** 2009-03-02 13:23:44.828  
**Elapsed:** 0 hr(s) 0 min(s) 1 sec(s) 327 ms  
**Total Warnings:** 8  
**Total Errors:** 6  
**No. of SeqIDs Defined:** 12  
**Actual SeqID Count:** 13

Error code	Error Description
E 201	Mandatory field data missing in <140>
E 201	Mandatory field data missing in <141>
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 323	Invalid/missing amino acid numbering SEQID (13)at Protein (209)
E 252	Calc# of Seq. differs from actual; 12 seqIDs defined; count=13

SEQUENCE LISTING

<110> Steinkasserer, Alexander

<120> Use of Soluble Forms of CD83 and Nucleic Acids Encoding them for the Treatment or Prevention of Diseases

<130> 032723woJH

<140> 10535522

<141> 2006-04-13

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

<211> 618

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(615)

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1 5 10 15

gct ccc gcg acg ccg gag gtg aag gtg gct tgc tcc gaa gat gtg gac 96  
Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp  
20 25 30

ttg ccc tgc acc gcc ccc tgg gat ccg cag gtt ccc tac acg gtc tcc 144  
Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser  
35 40 45

tgg gtc aag tta ttg gag ggt ggt gaa gag agg atg gag aca ccc cag 192  
Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln  
50 55 60

gaa gac cac ctc agg gga cag cac tat cat cag aag ggg caa aat ggt 240  
Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly  
65 70 75 80

tct ttc gac gcc ccc aat gaa agg ccc tat tcc ctg aag atc cga aac 288  
Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn  
85 90 95

act acc agc tgc aac tcg ggg aca tac agg tgc act ctg cag gac ccg 336  
Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro  
100 105 110

gat ggg cag aga aac cta agt ggc aag gtg atc ttg aga gtg aca gga 384  
Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly  
115 120 125

tgc cct gca cag cgt aaa gaa gag act ttt aag aaa tac aga gcg gag 432  
Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu

130	135	140	
att gtc ctg ctg ctg gct ctg gtt att ttc tac tta aca ctc atc att			480
Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile			
145	150	155	160
ttc act tgt aag ttt gca cgg cta cag agt atc ttc cca gat ttt tct			528
Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser			
165	170	175	
aaa gct ggc atg gaa cga gct ttt ctc cca gtt acc tcc cca aat aag			576
Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys			
180	185	190	
cat tta ggg cta gtg act cct cac aag aca gaa ctg gta tga			618
His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val			
195	200	205	
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<211> 205			
<212> PRT			
<213> Homo sapiens			
<400> 2			
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Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp			
20	25	30	
Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser			
35	40	45	
Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln			
50	55	60	
Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly			
65	70	75	80
Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn			
85	90	95	
Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro			
100	105	110	
Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly			
115	120	125	
Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu			
130	135	140	
Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile			
145	150	155	160
Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser			
165	170	175	

Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys  
180 185 190

His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val  
195 200 205

<210> 3  
<211> 2051  
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<213> Mus musculus  
<220>  
<221> CDS  
<222> (14)..(601)

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Met Ser Gln Gly Leu Gln Leu Leu Phe Leu Gly Cys  
1 5 10

gcc tgc agc ctg gca ccc gcg atg gcg atg cgg gag gtg acg gtg gct 97  
Ala Cys Ser Leu Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala  
15 20 25

tgc tcc gag acc gcc gac ttg cct tgc aca gcg ccc tgg gac ccg cag 145  
Cys Ser Glu Thr Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln  
30 35 40

ctc tcc tat gca gtg tcc tgg gcc aag gtc tcc gag agt ggc act gag 193  
Leu Ser Tyr Ala Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu  
45 50 55 60

agt gtg gag ctc ccg gag agc aag caa aac agc tcc ttc gag gcc ccc 241  
Ser Val Glu Leu Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro  
65 70 75

agg aga agg gcc tat tcc ctg acg atc caa aac act acc atc tgc agc 289  
Arg Arg Arg Ala Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser  
80 85 90

tcg ggc acc tac agg tgt gcc ctg cag gag ctc gga ggg cag cgc aac 337  
Ser Gly Thr Tyr Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn  
95 100 105

ttg agc ggc acc gtg gtt ctg aag gtg aca gga tgc ccc aag gaa gct 385  
Leu Ser Gly Thr Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala  
110 115 120

aca gag tca act ttc agg aag tac agg gca gaa gct gtg ttg ctc ttc 433  
Thr Glu Ser Thr Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe  
125 130 135 140

tct ctg gtt ttc tac ctg aca ctc atc att ttc acc tgc aaa ttt 481  
Ser Leu Val Val Phe Tyr Leu Thr Leu Ile Phe Thr Cys Lys Phe  
145 150 155

gca cga cta caa agc att ttc cca gat att tct aaa cct ggt acg gaa 529  
Ala Arg Leu Gln Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu  
160 165 170

caa gct ttt ctt cca gtc acc tcc cca agc aaa cat ttg ggg cca gtg 577  
Gln Ala Phe Leu Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val  
175 180 185

acc ctt cct aag aca gaa acg gta tgagtaggat ctccactggc ttttacaaag 631  
Thr Leu Pro Lys Thr Glu Thr Val  
190 195

ccaagggcac atcagatcag tgtgcctgaa tgccacccgg acaagagaag aatgagctcc 691

atcctcagat ggcaaccttt ctttgaagtc cttcacctga cagtgggctc cacactactc 751

cctgacacag ggtcttgagc accatcatat gatcacgaag catggagttt caccgcttct 811

ctgtggctgt cagcttaatg tttcatgtgg ctatctggc aacctcgtga gtgctttca 871

gtcatctaca agctatggtg agatgcaggt gaagcagggt catggaaat ttgaacactc 931

tgagctggcc ctgtgacaga ctccctgagga cagctgtctt ctccctacatc tgggatacat 991

ctctttgaat ttgtcctgtt tcgttgacc accccagatg tctcacatct ggcggaaatt 1051

gacaggccaa gctgtgagcc agtggaaat atttagcaa taatttccca gtgcgaaggt 1111

cctgcttta gtaaggagta ttatgtgtac atagaatga gaggtcagtg aactattccc 1171

cagcagggcc ttttcatctg gaaaagacat ccacaaaagc agcaatacag agggatgcca 1231

catttatttt ttaatcttc atgtacttgtt caaagaagaa tttttcatgt tttttcaaag 1291

aagtgtgttt ctttcctttt ttaaaatatg aaggtctagt tacatagcat tgctagctga 1351

caagcagcct gagagaagat ggagaatgtt cctcaaaata gggacagcaa gctagaagca 1411

ctgtacagt ccctgctggg aagggcagac aatggactga gaaaccagaa gtctggccac 1471

aagattgtct gtatgattct ggacgagtca cttgtggttt tcactctctg gttagtaaac 1531

cagatagttt agtctgggtt gaatacaatg gatgtgaagt tgcttgggaa aagctgaatg 1591

tagtgaatac attggcaact ctactggcgtt gttacccctgt tgatatccta gagttctgga 1651

gctgagcgaa tgcctgtcat atctcagttt gcccataat ccaaacacag gaggctacaa 1711

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gcgccttgcg cttgaaggac taatcacaag ttcttgaaga tatggaccta ggggagctat 1831

tgcggccacga caggaggaag ttctcagatg ttgcattgtat gtaacattgt tgcatttctt 1891

taatgagctg ggctccttcc tcatttgctt cccaaagaga ttttgcctt ctaatgggtgt 1951

gccccatcacc cacactatga aagtaaaagg gatgctgagc agatacagcg tgcttaccc 2011

tcagccatga ctttcatgct attaaaagaa tgcgttgaa 2051

<210> 4

<211> 196

<212> PRT

<213> Mus musculus

<400> 4

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20 25 30

Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Leu Ser Tyr Ala  
35 40 45

Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu Ser Val Glu Leu  
50 55 60

Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro Arg Arg Arg Ala  
65 70 75 80

Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser Ser Gly Thr Tyr  
85 90 95

Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu Ser Gly Thr  
100 105 110

Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala Thr Glu Ser Thr  
115 120 125

Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe Ser Leu Val Val  
130 135 140

Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln  
145 150 155 160

Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln Ala Phe Leu  
165 170 175

Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val Thr Leu Pro Lys  
180 185 190

Thr Glu Thr Val  
195

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<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for CD83ext

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31

<210> 6

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer for CD83ext

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aatttagaatt ctcaaattctc cgctctgtat t

31

<210> 7

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: partial  
sequence of pGEX2ThCD83ext

<220>

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<222> (1)..(417)

<220>

<221> mat\_peptide

<222> (28)..(417)

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48

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-5

-1 1

5

gtg aag gtg gct tgc tcc gaa gat gtg gac ttg ccc tgc acc gcc ccc

96

Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro

10

15

20

tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag

144

Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu

25

30

35

ggt ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga

192

Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly

40

45

50

55

cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat

240

Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn

60

65

70

gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg

288

Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser

75

80

85

ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta

336

Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu  
 90 95 100  
 agt ggc aag gtg atc ttg aga gtg aca gga tgc cct gca cag cgt aaa 384  
 Ser Gly Lys Val Ile Leu Arg Val Thr Gly Cys Pro Ala Gln Arg Lys  
 105 110 115  
 gaa gag act ttt aag aaa tac aga gcg gag att tgagaattca tcgtgact 435  
 Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile  
 120 125 130  
  
 <210> 8  
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 <212> PRT  
 <213> Artificial Sequence  
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 10 15 20  
 Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu  
 25 30 35  
 Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly  
 40 45 50 55  
 Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn  
 60 65 70  
 Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser  
 75 80 85  
 Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu  
 90 95 100  
 Ser Gly Lys Val Ile Leu Arg Val Thr Gly Cys Pro Ala Gln Arg Lys  
 105 110 115  
 Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile  
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<222> (1)..(417)

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gtg aag gtg gct tgc tcc gaa gat gtg gac ttg ccc tgc acc gcc ccc 96  
Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro  
10 15 20

tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag 144  
Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu  
25 30 35

ggt ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga 192  
Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly  
40 45 50 55

cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat 240  
Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn  
60 65 70

gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg 288  
Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser  
75 80 85

ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta 336  
Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu  
90 95 100

agt ggc aag gtg atc ttg aga gtg aca gga tcc cct gca cag cgt aaa 384  
Ser Gly Lys Val Ile Leu Arg Val Thr Gly Ser Pro Ala Gln Arg Lys  
105 110 115

gaa gag act ttt aag aaa tac aga gcg gag att tgagaattca tcgtgact 435  
Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile  
120 125 130

<210> 10

<211> 139

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: partial  
sequence of pGEX2ThCD83ext\_mut129\_CtoS

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Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Thr Pro Glu  
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Val Lys Val Ala Cys Ser Glu Asp Val Asp Le